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Supplemental Material

Prenatal Air Pollution Exposures, DNA Methyl Transferase Genotypes, and Associations with Newborn LINE1 and Alu Methylation and Childhood Blood Pressure and Carotid Intima-Media Thickness in the Children's Health Study

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Table S3. Association between a 1 % increase in LINE1 (N=411) and AluYb8 (N=190) methylation and CIMT and blood pressure

Table S4. SNPs and 1st trimester air pollutants showing joint effects on cardiovascular phenotypes

Figure S1. Boxplots of percent methylation for each assayed CpG in a) LINE1 (N=392) and b) AluYb8 (N=181). Boxes extend from the 25th to the 75th percentile, horizontal bars represent the median, whiskers extend 1.5 times the length of the interquartile range (IQR) above and below the 75th and 25th percentiles, respectively, and outliers beyond whiskers are represented as points.

Figure S2. Distributions of ambient air pollutants by trimester (N=392). Boxes extend from the 25th to the 75th percentile, horizontal bars represent the median, whiskers extend 1.5 times the length of the interquartile range (IQR) above and below the 75th and 25th percentiles, respectively, and outliers are represented as points.

Figure S3. Illustration of rs16999714 (yellow bar) upstream of the DNMT1 transcription start site in a putative enhancer that appears a) inactive in H1 BMP4 derived mesendoderm cells, b) active in H1 BMP4 derived trophoblast cells, and c) adjacent to a poised enhancer in H1 derived mesenchymal stem cells. Blue is H3K27ac and green is H3K4me1. The figure was produced using the Wash U Epigenome Browser.

Reference

Additional Files

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Supplemental Code and Data Zip File Index

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Excel File S2. Results for all SNP-1st trimester air pollutant interaction tests using a generalized linear regression model in which SNPs were treated as ordinal variables